IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant	:	Eaton, et al.
Appl. No.	:	10/063,534
Filed	:	May 2, 2002
For	:	ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID OVEREXPRESSED IN KIDNEY TUMOR AND UNDEREXPRESSED IN LUNG TUMOR (as amended)
Examiner	:	Seharaseyon, J.
Group Art Unit	:	1647

CERTIFICATE OF MAILING

I hereby certify that this correspondence and all marked attachments are being deposited with the United States Postal Service as first-class mail in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on

September 2, 2004
(Date)

AnneMarie Kaiser, Reg. No. 37,649

RESPONSE TO NOTICE TO COMPLY

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

This Response to the Notice to Comply conforms the Sequence Listing to the rules of practice specified by the United States Patent and Trademark Office. Submitted herewith is a paper copy of the Sequence Listing and a copy of the Notice to Comply.

Please enter the attached sequence listing in the above-referenced application.

VERIFICATION UNDER 37 C.F.R. §1.821(f) & (g)

The sequences appearing in the attached Sequence Listing were included in the application as filed. Pursuant to 37 C.F.R. §1.821(g), no new matter is being added herewith. As required under 37 C.F.R. §1.821(f), I hereby verify that the data on the disk previously submitted and the paper copy of the Sequence Listing are identical.

Applicants believe this response to Notice to Comply brings the present application into compliance with the Sequence Listing requirements. A copy of the Notice to Comply is also submitted herewith.

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: Sept. 2, 2004

By: _____
AnneMarie Kaiser
Registration No. 37,649
Attorney of Record
Customer No. 30,313
(619) 235-8550

S:\DOCS\BSG\BSG-1357.DOC
081304

COPY

Notice to Comply	Application No. 10/063 534	Applicant(s) EATON ET AL
	Examiner J. Schwaseym	Art Unit 1647

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other:

Applicant Must Provide:

☐ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216 or (703) 308-2923
For CRF Submission Help, call (703) 308-4212 or 308-2923
PatentIn Software Program Support
Technical Assistance.....703-287-0200
To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

GenBank (Release 142, jun 2004)

494 100 0.0
P_AAF92072 Human PRO831 cDNA. 494 bp, cDNA, PAT 15-MAY-2001
ACCESSION P_AAF92072
KEYWORDS GENESEQ; Human; PRO protein; mapping; patent; patentdb (v200414, 01-JUL-2004).
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 494)
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J. Grimaldi,C.J., Gurney,A.L., Watanabe,C.K., Wood,W.I.
TITLE Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
JOURNAL Patent: WO200116318-A2; Filing Date: 24-AUG-2000; 2000WO-US023328; Publication Date: 08-MAR-2001; Priority: 01-SEP-1999; 99WO-US020111. 15-SEP-1999; 99WO-US021090. 07-DEC-1999; 99US-0169495P. 09-DEC-1999; 99US-0170262P. 11-JAN-2000; 2000US-0175481P. 18-FEB-2000; 2000WO-US004341. 18-FEB-2000; 2000WO-US004342. 22-FEB-2000; 2000WO-US004414. 01-MAR-2000; 2000WO-US005601. 03-MAR-2000; 2000US-0187202P. 21-MAR-2000; 2000US-0191007P. 30-MAR-2000; 2000WO-US008439. 25-APR-2000; 2000US-0199397P. 22-MAY-2000; 2000WO-US014042. 05-JUN-2000; 2000US-0209832P; Assignee: (GETH) GENENTECH INC; Cross Reference: WPI; 2001-183260/18. P-PSDB; AAB87540; Patent Format: Claim 2; Fig 29; 278pp; English.
COMMENT The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping
FEATURES Location/Qualifiers
BASE COUNT 128 a 111 c 120 g 135 t
ORIGIN

494 100 0.0
AX092298 Sequence 29 from Patent WO0116318. 494 bp, DNA, linear, PAT 21-MAR-2001
ACCESSION AX092298
VERSION AX092298.1 GI:13444463
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

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  JOURNAL   Patent: WO 0116318-A 29 08-MAR-2001;
          Genentech, Inc. (US)
FEATURES             Location/Qualifiers
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BASE COUNT
ORIGIN

493 100   0.0
P_AAA37028  Human PRO831 (UNQ471) cDNA sequence SEQ ID NO:21. 493 bp,
          cDNA, PAT 08-AUG-2000
ACCESSION   P_AAA37028
KEYWORDS    GENESEQ; Human; PRO polypeptide; membrane bound protein; receptor;
          diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical;
          screening;  patent; patentdb (v200414, 01-JUL-2004).
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens.
REFERENCE   1  (bases 1 to 493)
  AUTHORS   Baker,K.,  Goddard,A.,  Gurney,A.L.,  Smith,V.,  Watanabe,C.K.,
          Wood,W.I.
  TITLE     New mammalian DNA sequences encoding transmembrane, receptor or
          secreted  PRO polypeptides, useful for screening of potential
          peptide or small  molecule inhibitors of the relevant
          receptor/ligand interactions.
  JOURNAL   Patent: WO200012708-A2; Filing Date: 01-SEP-1999;  99WO-US020111;
          Publication Date: 09-MAR-2000; Priority: 01-SEP-1998;
          98US-0098716P. 01-SEP-1998;   98US-0098749P. 01-SEP-1998;
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          98US-0099536P. 09-SEP-1998;   98US-0099596P. 09-SEP-1998;
          98US-0099598P. 09-SEP-1998;   98US-0099602P. 09-SEP-1998;
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          98US-0099754P. 10-SEP-1998;   98US-0099763P. 10-SEP-1998;
          98US-0099792P. 10-SEP-1998;   98US-0099808P. 10-SEP-1998;
          98US-0099812P. 10-SEP-1998;   98US-0099815P. 10-SEP-1998;
          98US-0099816P. 15-SEP-1998;   98US-0100385P. 15-SEP-1998;
          98US-0100388P. 15-SEP-1998;   98US-0100390P. 16-SEP-1998;
          98US-0100584P. 16-SEP-1998;   98US-0100627P. 16-SEP-1998;
          98US-0100661P. 16-SEP-1998;   98US-0100662P. 16-SEP-1998;
          98US-0100664P. 17-SEP-1998;   98US-0100683P. 17-SEP-1998;
          98US-0100684P. 17-SEP-1998;   98US-0100710P. 17-SEP-1998;
          98US-0100711P. 17-SEP-1998;   98US-0100919P. 17-SEP-1998;
          98US-0100930P. 18-SEP-1998;   98US-0100848P. 18-SEP-1998;
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          98US-0101068P. 18-SEP-1998;   98US-0101071P. 22-SEP-1998;
          98US-0101279P. 23-SEP-1998;   98US-0101471P. 23-SEP-1998;
          98US-0101472P. 23-SEP-1998;   98US-0101474P. 23-SEP-1998;
          98US-0101475P. 23-SEP-1998;   98US-0101476P. 23-SEP-1998;
          98US-0101477P. 23-SEP-1998;   98US-0101479P. 24-SEP-1998;
          98US-0101738P. 24-SEP-1998;   98US-0101741P. 24-SEP-1998;
          98US-0101743P. 24-SEP-1998;   98US-0101915P. 24-SEP-1998;
          98US-0101916P. 29-SEP-1998;   98US-0102207P. 29-SEP-1998;
          98US-0102240P. 29-SEP-1998;   98US-0102307P. 29-SEP-1998;
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98US-0102570P. 30-SEP-1998; 98US-0102571P. 01-OCT-1998;
98US-0102684P. 01-OCT-1998; 98US-0102687P. 02-OCT-1998;
98US-0102965P. 06-OCT-1998; 98US-0103258P. 06-OCT-1998;
98US-0103449P. 07-OCT-1998; 98US-0103314P. 07-OCT-1998;
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98US-0103395P. 07-OCT-1998; 98US-0103396P. 07-OCT-1998;
98US-0103401P. 08-OCT-1998; 98US-0103633P. 08-OCT-1998;
98US-0103678P. 08-OCT-1998; 98US-0103679P. 08-OCT-1998;
98US-0103711P. 14-OCT-1998; 98US-0104257P. 20-OCT-1998;
98US-0104987P. 20-OCT-1998; 98US-0105000P. 20-OCT-1998;
98US-0105002P. 21-OCT-1998; 98US-0105104P. 22-OCT-1998;
98US-0105169P. 22-OCT-1998; 98US-0105266P. 26-OCT-1998;
98US-0105693P. 26-OCT-1998; 98US-0105694P. 27-OCT-1998;
98US-0105807P. 27-OCT-1998; 98US-0105881P. 27-OCT-1998;
98US-0105882P. 27-OCT-1998; 98US-0106062P. 28-OCT-1998;
98US-0106023P. 28-OCT-1998; 98US-0106029P. 28-OCT-1998;
98US-0106030P. 28-OCT-1998; 98US-0106032P. 28-OCT-1998;
98US-0106033P. 28-OCT-1998; 98US-0106178P. 29-OCT-1998;
98US-0106248P. 29-OCT-1998; 98US-0106384P. 29-OCT-1998;
98US-0108500P. 30-OCT-1998; 98US-0106464P. 03-NOV-1998;
98US-0106856P. 03-NOV-1998; 98US-0106902P. 03-NOV-1998;
98US-0106905P. 03-NOV-1998; 98US-0106919P. 03-NOV-1998;
98US-0106932P. 03-NOV-1998; 98US-0106934P. 10-NOV-1998;
98US-0107783P. 17-NOV-1998; 98US-0108775P. 17-NOV-1998;
98US-0108779P. 17-NOV-1998; 98US-0108787P. 17-NOV-1998;
98US-0108788P. 17-NOV-1998; 98US-0108801P. 17-NOV-1998;
98US-0108802P. 17-NOV-1998; 98US-0108806P. 17-NOV-1998;
98US-0108807P. 17-NOV-1998; 98US-0108867P. 17-NOV-1998;
98US-0108925P. 18-NOV-1998; 98US-0108848P. 18-NOV-1998;
98US-0108849P. 18-NOV-1998; 98US-0108850P. 18-NOV-1998;
98US-0108851P. 18-NOV-1998; 98US-0108852P. 18-NOV-1998;
98US-0108858P. 18-NOV-1998; 98US-0108904P; Assignee: (GETH)
GENENTECH INC; Cross Reference: WPI; 2000-237871/20. P-PSDB;
AAY99346; Patent Format: Claim 2; Fig 13; 773pp; English.

COMMENT AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention

FEATURES Location/Qualifiers
BASE COUNT 127 a 111 c 120 g 135 t
ORIGIN

486 100 0.0
BC021104 Homo sapiens apelin, AGTRL1 ligand, mRNA (cDNA clone MGC:31846 IMAGE:4586949), complete cds. 2673 bp, mRNA, linear, PRI 30-JUN-2004
ACCESSION BC021104
VERSION BC021104.1 GI:18088893
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2673)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

REFERENCE 2 (bases 1 to 2673)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 40 Row: f Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21314667.

FEATURES Location/Qualifiers
source 1..2673
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BASE COUNT
ORIGIN

468 100   0.0
P_AAX235184Human kidney aminopeptidase P genomic DNA fragment 2. 998 bp,
          DNA, PAT 23-JUN-1999
ACCESSION   P_AAX23518
KEYWORDS    GENESEQ; Aminopeptidase; human; AmP; gene therapy; treatment;
          AmP-deficiency; prenatal diagnosis; angioedema; antihypertensive
          agent; atherosclerosis; arterial stenosis; industrial protein feed;
          malabsorption syndrome; proteinaceous waste degradation; additive;
          immunohistochemistry;  patent; patentdb (v200414, 01-JUL-2004).
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens.
REFERENCE   1  (bases 1 to 49998)
  AUTHORS   Ryan,J.W.,  Sprinkle,T.J.C.,  Venema,R.C.
  TITLE     Nucleic acid encoding human aminopeptidase P.
  JOURNAL   Patent: WO9911799-A2; Filing Date: 02-SEP-1998;   98WO-US018426;
          Publication Date: 11-MAR-1999; Priority: 02-SEP-1997;
          97US-0057854P; Assignee: (MEDI-) MEDICAL COLLEGE GEORGIA RES INST;
          Cross Reference: WPI; 1999-205193/17; Patent Format: Claim 13; Page
          109-139; 201pp; English.
COMMENT     This invention describes the isolation of a novel human
          aminopeptidase P  (AmP). This protein is used to produce recombinant
          AmP and can be used  for gene therapy for treating AmP-deficiency
          conditions. Its fragments  are used as primers and probes to
          identify patients with homozygous and  heterozygous AmP deficiency,
          including prenatal diagnosis (patients  defective in AmP are at risk
          of developing angioedema if treated with  angiotensin-converting
          enzyme inhibitors), also as antisense inhibitors  in cases of
          excessive AmP expression. The product of the invention is  also used
          to identify AmP-expressing sequences in other animals and to
          generate transgenic animals, and comparisons of genomic sequences
          are  used to detect mutations. AmP inhibitors are potentially useful
          as  antihypertensive agents and to prevent or treat arterial
          (re)stenosis or  atherosclerosis. The structure of AmP is used to
          design synthetic  substrates, e.g. for use in AmP assays. AmP, which
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hydrolyzes N-terminal imido bonds, can be used to degrade industrial protein feeds to free amino acids, to degrade proteinaceous wastes, as additives in enzyme formulations used to treat malabsorption syndrome and for studying its biological role. Antibodies against AmP are used in immunohistochemical methods to study AmP distribution
FEATURES Location/Qualifiers
BASE COUNT 12605 a 11725 c 11351 g 14317 t
ORIGIN

468 100 0.0
HS454M7 Human DNA sequence from clone RP3-454M7 on chromosome Xq25-26.3, complete sequence. 151152 bp, DNA, linear, PRI 05-JUN-2003
ACCESSION AL022162
VERSION AL022162.1 GI:3171881
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 151152)
AUTHORS Pavitt,R.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Jun 2, 1998 this sequence version replaced gi:2969945.
---------- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality }= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
RP3-454M7 is from the library RPCI-3 constructed by the group of

```
          Pieter de Jong. For further details see
          http://www.chori.org/bacpac/home.htm
          VECTOR: pCYPAC2
          This sequence is the entire insert of clone RP3-454M7.
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                     /clone="RP3-454M7"
                     /clone_lib="RPCI-3"
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                     10696..10805,12706..12841,18582..18692,19339..19504,
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                     33287..33398,33588..35998)
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                     /product="dJ454M7.1.1 (Lowe Oculocerebrorenal Syndrome)"
                     /note="variant 1
                     match: cDNAs: Em:M88162 Em:U57627 Em:M74161 Em:AF040094
                     match: ESTs: Em:AA368192 Em:AA704671 Em:AA515789
                     Em:AA102623 Em:AA126320 Em:T63686 Em:AA884344 Em:N92504
                     Em:AA044611 Em:AA188493 Em:AA743649 Em:AA836673 Em:R67320
                     Em:AA100629 Em:AA085500 Em:R94403 Em:AA056506 Em:AA034375
                     Em:AA142870 Em:AA150871 Em:T84251 Em:AA122020 Em:AA906612
                     Em:F07337 Em:AA628152 Em:AA878369 Em:AA640853 Em:AA189134
                     Em:AA044666 Em:AA740555 Em:R18793 Em:AA844284 Em:AA904845
                     Em:AA042798 Em:AA122019 Em:H53971 Em:W38961 Em:AA805220
                     Em:AA868822 Em:AA032176 Em:AA034374 Em:T84250 Em:N56932
                     Em:AA169401 Em:AA188849 Em:N46002 Em:AA056392 Em:H87857
                     Em:W52373 Em:AA587050 Em:AA100630 Em:T88888 Em:H27722
                     Em:AA186750 Em:R66483 Em:T28294"
                     /evidence=not_experimental
     CDS             join(<769..877,1303..1392,2075..2195,2282..2443,
                     3992..4093,4621..4735,5826..5942,6041..6228,9214..9325,
                     10696..10805,12706..12841,18582..18692,19339..19504,
                     19759..19994,27786..27809,30444..30560,31621..31705,
                     32328..32455,33287..33398,33588..33712)
                     /gene="OCRL1"
                     /codon_start=1
                     /evidence=not_experimental
                     /product="dJ454M7.1.2 (variant 2)"
                     /protein_id="CAA18150.1"
                     /db_xref="GI:3171882"
     CDS             join(<769..877,1303..1392,2075..2195,2282..2443,
                     3992..4093,4621..4735,5826..5942,6041..6228,9214..9325,
                     10696..10805,12706..12841,18582..18692,19339..19504,
                     19759..19994,30444..30560,31621..31705,32328..32455,
                     33287..33398,33588..33712)
                     /gene="OCRL1"
                     /note="variant 1"
                     /codon_start=1
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                     /evidence=not_experimental
                     /product="dJ454M7.1.1 (Lowe Oculocerebrorenal Syndrome)"
                     /protein_id="CAA18151.1"
                     /db_xref="GI:4160528"
     repeat_region   1586..1847
                     /note="MIR repeat: matches 2..262 of consensus"
     repeat_region   2642..2940
                     /note="AluJb repeat: matches 1..302 of consensus"
     repeat_region   6639..6933
                     /note="MER33 repeat: matches 1..323 of consensus"
     repeat_region   7178..8315
                     /note="L1PA2 repeat: matches 5000..6146 of consensus"
     repeat_region   11225..11294
                     /note="MER5B repeat: matches 109..178 of consensus"
     repeat_region   11345..11657
                     /note="AluYb8 repeat: matches 1..310 of consensus"
     repeat_region   11736..11797
                     /note="31 copies 2 mer tt 72% conserved"
     repeat_region   12436..12562
                     /note="L2 repeat: matches 2579..2710 of consensus"
     repeat_region   13276..13457
                     /note="AluSg/x repeat: matches 129..310 of consensus"
     repeat_region   13679..13873
                     /note="MIR repeat: matches 5..213 of consensus"
     repeat_region   14132..14206
                     /note="MIR repeat: matches 163..233 of consensus"
     repeat_region   14207..14413
                     /note="MER8 repeat: matches 2..239 of consensus"
     repeat_region   14414..14548
                     /note="MIR repeat: matches 12..163 of consensus"
     repeat_region   14793..15073
                     /note="AluY repeat: matches 1..311 of consensus"
     repeat_region   15383..15589
                     /note="MER3 repeat: matches 1..209 of consensus"
     repeat_region   16139..16279
                     /note="MER5B repeat: matches 29..178 of consensus"
     repeat_region   16317..16466
                     /note="MIR repeat: matches 52..212 of consensus"
     repeat_region   16667..17000
                     /note="L1PA9 repeat: matches 5829..6163 of consensus"
     repeat_region   17001..17301
                     /note="AluYb8 repeat: matches 1..302 of consensus"
     repeat_region   17302..17642
                     /note="L1PA9 repeat: matches 5491..5829 of consensus"
     repeat_region   18285..18620
                     /note="2 copies 168 mer 78% conserved"
     repeat_region   18772..18981
                     /note="MIR repeat: matches 6..242 of consensus"
     repeat_region   18945..19005
                     /note="L2 repeat: matches 2648..2702 of consensus"
     repeat_region   20349..20489
                     /note="MIR repeat: matches 1..150 of consensus"
     repeat_region   20543..20697
                     /note="MER5A repeat: matches 22..188 of consensus"
     repeat_region   21496..21830
                     /note="L1MC4 repeat: matches 7477..7849 of consensus"
     repeat_region   22420..22650
```

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                     /note="MER46A repeat: matches 1..236 of consensus"
     repeat_region   22894..22965
                     /note="3 copies 24 mer 83% conserved"
     repeat_region   24309..24606
                     /note="AluSx repeat: matches 1..299 of consensus"
     repeat_region   25081..25134
                     /note="27 copies 2 mer ta 70% conserved"
     repeat_region   25168..25193
                     /note="13 copies 2 mer tg 100% conserved"
     repeat_region   25262..25301
                     /note="20 copies 2 mer tc 90% conserved"
     repeat_region   25302..25642
                     /note="L2 repeat: matches 2078..2419 of consensus"
     repeat_region   26542..26704
                     /note="MIR repeat: matches 1..160 of consensus"
     repeat_region   26822..27057
                     /note="MIR repeat: matches 8..255 of consensus"
     repeat_region   28330..28399
                     /note="MIR repeat: matches 82..151 of consensus"
     repeat_region   30715..30819
                     /note="MIR repeat: matches 35..138 of consensus"
     repeat_region   31196..31319
                     /note="AluJb repeat: matches 2..125 of consensus"
     repeat_region   37202..37675
                     /note="L2 repeat: matches 1597..2041 of consensus"
     repeat_region   37676..37990
                     /note="AluJb repeat: matches 1..312 of consensus"
     repeat_region   37991..38142
                     /note="L2 repeat: matches 2041..2182 of consensus"
     repeat_region   38143..38316
                     /note="MER5A repeat: matches 3..189 of consensus"
     repeat_region   38317..38464
                     /note="L2 repeat: matches 2182..2419 of consensus"
     repeat_region   38676..38801
                     /note="MIR repeat: matches 11..134 of consensus"
     repeat_region   38858..38984
                     /note="MIR repeat: matches 123..257 of consensus"
     repeat_region   39284..39886
                     /note="L2 repeat: matches 2147..2748 of consensus"
     repeat_region   39913..40014
                     /note="MIR repeat: matches 175..262 of consensus"
     repeat_region   40015..40311
                     /note="AluSg repeat: matches 1..297 of consensus"
     repeat_region   40312..40428
                     /note="MIR repeat: matches 14..175 of consensus"
     repeat_region   40667..40774
                     /note="L2 repeat: matches 2616..2702 of consensus"
     repeat_region   40776..41088
                     /note="AluSx repeat: matches 1..305 of consensus"
     repeat_region   41528..41936
                     /note="L2 repeat: matches 2267..2709 of consensus"
     repeat_region   42180..42713
                     /note="L1MB3 repeat: matches 5584..6153 of consensus"
     repeat_region   42714..43014
                     /note="AluJb repeat: matches 1..312 of consensus"
     repeat_region   43015..43042
                     /note="L1MB3 repeat: matches 6153..6178 of consensus"
```

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repeat_region   43197..43238
                /note="5S repeat: matches 1..42 of consensus"
repeat_region   43282..43574
                /note="L2 repeat: matches 2405..2677 of consensus"
repeat_region   45284..45741
                /note="MLT1C repeat: matches 1..466 of consensus"
repeat_region   45835..45905
                /note="L2 repeat: matches 1139..1203 of consensus"
repeat_region   45906..46207
                /note="AluSq repeat: matches 12..313 of consensus"
repeat_region   46208..46584
                /note="L2 repeat: matches 1203..1621 of consensus"
repeat_region   46714..47015
                /note="AluSg repeat: matches 1..302 of consensus"
repeat_region   47016..47159
                /note="MER58B repeat: matches 196..341 of consensus"
repeat_region   47168..47374
                /note="MER30 repeat: matches 1..230 of consensus"
repeat_region   47427..47581
                /note="MER61A repeat: matches 4..158 of consensus"
repeat_region   47611..47774
                /note="AluSx repeat: matches 12..175 of consensus"
repeat_region   48682..48987
                /note="AluY repeat: matches 1..306 of consensus"
repeat_region   49541..49678
                /note="L2 repeat: matches 1906..2046 of consensus"
repeat_region   49698..49898
                /note="MER53 repeat: matches 1..188 of consensus"
repeat_region   49909..49978
                /note="LTR19B repeat: matches 59..140 of consensus"
repeat_region   50220..50423
                /note="L2 repeat: matches 2518..2730 of consensus"
repeat_region   50421..50492
                /note="3 copies 24 mer 93% conserved"
repeat_region   50846..50915
                /note="MIR repeat: matches 48..117 of consensus"
repeat_region   50914..51068
                /note="MIR repeat: matches 34..211 of consensus"
repeat_region   51124..51292
                /note="AluSg/x repeat: matches 130..300 of consensus"
repeat_region   51517..51587
                /note="MER96 repeat: matches 105..175 of consensus"
repeat_region   52716..52853
                /note="MIR repeat: matches 68..213 of consensus"
repeat_region   52994..53224
                /note="MIR repeat: matches 2..258 of consensus"
repeat_region   54036..54154
                /note="MLT1I repeat: matches 292..410 of consensus"
repeat_region   54234..54586
                /note="MLT1A2 repeat: matches 1..373 of consensus"
repeat_region   54612..54704
                /note="MLT1J repeat: matches 106..200 of consensus"
repeat_region   54708..54755
                /note="L2 repeat: matches 2691..2738 of consensus"
repeat_region   55103..55409
                /note="AluYb8 repeat: matches 1..314 of consensus"
repeat_region   55876..56326
```

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                     /note="L2 repeat: matches 2225..2658 of consensus"
repeat_region        56404..56697
                     /note="AluSg repeat: matches 1..292 of consensus"
repeat_region        56760..56882
                     /note="L2 repeat: matches 2605..2730 of consensus"
repeat_region        57036..57226
                     /note="MIR repeat: matches 73..262 of consensus"
repeat_region        57448..57579
                     /note="L1PA16 repeat: matches 6025..6157 of consensus"
repeat_region        57817..58128
                     /note="L2 repeat: matches 2434..2746 of consensus"
repeat_region        58772..59030
                     /note="MIR repeat: matches 1..262 of consensus"
repeat_region        59040..59091
                     /note="MIR repeat: matches 206..257 of consensus"
repeat_region        59050..59118
                     /note="L2 repeat: matches 2626..2729 of consensus"
repeat_region        59465..59797
                     /note="AluSx repeat: matches 1..301 of consensus"
repeat_region        61554..61833
                     /note="AluSx repeat: matches 6..286 of consensus"
repeat_region        62011..62239
                     /note="MIR repeat: matches 2..242 of consensus"
repeat_region        62265..62379
                     /note="L2 repeat: matches 2430..2545 of consensus"
repeat_region        63472..63529
                     /note="MIR repeat: matches 185..242 of consensus"
repeat_region        64262..64313
                     /note="MIR repeat: matches 92..143 of consensus"
repeat_region        64330..64409
                     /note="MER33 repeat: matches 241..324 of consensus"
repeat_region        64459..64631
                     /note="L1MA10 repeat: matches 5999..6322 of consensus"
repeat_region        64637..64862
                     /note="MER33 repeat: matches 5..225 of consensus"
repeat_region        65788..66082
                     /note="AluJo repeat: matches 6..304 of consensus"
repeat_region        66968..66991
                     /note="L2 repeat: matches 2470..2493 of consensus"
repeat_region        67036..67653
                     /note="L2 repeat: matches 1882..2511 of consensus"
repeat_region        67654..67700
                     /note="L1PA16 repeat: matches 4148..4193 of consensus"
repeat_region        67701..67998
                     /note="AluY repeat: matches 1..296 of consensus"
repeat_region        67999..68463
                     /note="L1PA16 repeat: matches 4193..4655 of consensus"
repeat_region        68464..68826
                     /note="THE1B repeat: matches 1..364 of consensus"
repeat_region        68827..70335
                     /note="L1PA16 repeat: matches 4655..6143 of consensus"
repeat_region        70349..70538
                     /note="L2 repeat: matches 1697..1895 of consensus"
repeat_region        70565..70865
                     /note="AluY repeat: matches 1..305 of consensus"
repeat_region        70932..71126
                     /note="L1ME3 repeat: matches 5734..5939 of consensus"
```

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repeat_region   71385..71690
                /note="AluYa5 repeat: matches 1..310 of consensus"
repeat_region   71717..72253
                /note="MLT1F repeat: matches 11..513 of consensus"
repeat_region   72615..72631
                /note="MIR repeat: matches 196..212 of consensus"
repeat_region   72632..72870
                /note="MER8 repeat: matches 1..239 of consensus"
repeat_region   72871..73028
                /note="MIR repeat: matches 45..196 of consensus"
repeat_region   73892..73979
                /note="MIR repeat: matches 59..147 of consensus"
repeat_region   74431..74484
                /note="27 copies 2 mer ca 96% conserved"
repeat_region   74436..74483
                /note="2 copies 24 mer 100% conserved"
repeat_region   74504..74671
                /note="MIR repeat: matches 2..171 of consensus"
repeat_region   75019..75185
                /note="L2 repeat: matches 2517..2704 of consensus"
repeat_region   75149..75249
                /note="MIR repeat: matches 28..137 of consensus"
repeat_region   75397..75588
                /note="MLT1A1 repeat: matches 1..194 of consensus"
repeat_region   75646..75831
                /note="MLT1A1 repeat: matches 171..365 of consensus"
repeat_region   76554..76826
                /note="AluSg1 repeat: matches 1..308 of consensus"
repeat_region   76863..76903
                /note="L2 repeat: matches 2652..2693 of consensus"
repeat_region   77089..77189
                /note="MIR repeat: matches 41..144 of consensus"
repeat_region   77359..77679
                /note="AluSx repeat: matches 1..301 of consensus"
repeat_region   78584..78722
                /note="L2 repeat: matches 2615..2750 of consensus"
repeat_region   79058..79304
                /note="MIR repeat: matches 8..262 of consensus"
repeat_region   81458..81515
                /note="MIR repeat: matches 95..154 of consensus"
repeat_region   81526..81665
                /note="L2 repeat: matches 2352..2503 of consensus"
repeat_region   81793..81843
                /note="L2 repeat: matches 2706..2750 of consensus"
repeat_region   82019..82082
                /note="MIR repeat: matches 90..153 of consensus"
repeat_region   82664..82739
                /note="L2 repeat: matches 2647..2722 of consensus"
repeat_region   82740..83045
                /note="AluSx repeat: matches 1..312 of consensus"
repeat_region   83046..83071
                /note="L2 repeat: matches 2722..2747 of consensus"
repeat_region   83813..83946
                /note="MIR repeat: matches 89..250 of consensus"
repeat_region   83904..83954
                /note="L2 repeat: matches 2648..2698 of consensus"
repeat_region   83963..84024
```

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                     /note="MIR repeat: matches 77..140 of consensus"
repeat_region        84133..84258
                     /note="MIR repeat: matches 7..136 of consensus"
repeat_region        84602..84697
                     /note="MIR repeat: matches 49..135 of consensus"
repeat_region        85012..85350
                     /note="MLT1A2 repeat: matches 1..340 of consensus"
repeat_region        85365..85456
                     /note="MIR repeat: matches 33..128 of consensus"
repeat_region        85526..85776
                     /note="MIR repeat: matches 7..262 of consensus"
repeat_region        85935..86011
                     /note="MER58A repeat: matches 42..121 of consensus"
repeat_region        86101..86173
                     /note="MER58A repeat: matches 143..219 of consensus"
repeat_region        87299..87643
                     /note="AluYb8 repeat: matches 1..310 of consensus"
repeat_region        88003..88303
                     /note="AluSx repeat: matches 1..301 of consensus"
repeat_region        92655..92799
                     /note="L1MC5 repeat: matches 7720..7866 of consensus"
repeat_region        99017..99109
                     /note="L2 repeat: matches 2388..2488 of consensus"
repeat_region        99392..99521
                     /note="L2 repeat: matches 2576..2710 of consensus"
repeat_region        99694..99834
                     /note="L2 repeat: matches 2610..2750 of consensus"
repeat_region        100051..100090
                     /note="20 copies 2 mer tt 80% conserved"
repeat_region        100093..100400
                     /note="AluSx repeat: matches 3..312 of consensus"
repeat_region        100764..100931
                     /note="MER3 repeat: matches 3..207 of consensus"
repeat_region        101144..101446
                     /note="AluJo repeat: matches 1..292 of consensus"
repeat_region        101798..101867
                     /note="L2 repeat: matches 2672..2744 of consensus"
repeat_region        101952..102471
                     /note="MER1A repeat: matches 6..527 of consensus"
repeat_region        102850..103006
                     /note="MIR repeat: matches 20..168 of consensus"
repeat_region        103007..103052
                     /note="MLT1A1 repeat: matches 1..51 of consensus"
repeat_region        103053..103356
                     /note="AluSp repeat: matches 1..303 of consensus"
repeat_region        103357..103729
                     /note="MLT1A1 repeat: matches 51..365 of consensus"
repeat_region        103730..103791
                     /note="MIR repeat: matches 168..231 of consensus"
repeat_region        103886..103998
                     /note="MSTA repeat: matches 1..114 of consensus"
repeat_region        103996..104323
                     /note="MSTA repeat: matches 1..388 of consensus"
repeat_region        104372..104503
                     /note="AluY repeat: matches 166..297 of consensus"
repeat_region        104594..104824
                     /note="MIR repeat: matches 10..259 of consensus"
```

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repeat_region   104874..104954
                /note="L2 repeat: matches 2624..2709 of consensus"
repeat_region   105235..105332
                /note="MIR repeat: matches 47..145 of consensus"
repeat_region   107333..107459
                /note="MLT1C repeat: matches 340..466 of consensus"
repeat_region   107460..107589
                /note="L1MA7 repeat: matches 6159..6288 of consensus"
repeat_region   107590..107718
                /note="MLT1C repeat: matches 211..340 of consensus"
repeat_region   107755..108017
                /note="AluJo repeat: matches 18..277 of consensus"
repeat_region   108019..108208
                /note="MLT1C repeat: matches 1..192 of consensus"
repeat_region   108326..108922
                /note="L2 repeat: matches 2080..2710 of consensus"
repeat_region   109592..109635
                /note="22 copies 2 mer gg 75% conserved"
repeat_region   110302..110511
                /note="L1MA10 repeat: matches 5970..6317 of consensus"
repeat_region   110589..111071
                /note="L1ME1 repeat: matches 5477..5952 of consensus"
repeat_region   111077..111135
                /note="L1MB4 repeat: matches 6124..6183 of consensus"
repeat_region   111153..111414
                /note="L1MB3 repeat: matches 5909..6182 of consensus"
repeat_region   111419..111617
                /note="L1ME1 repeat: matches 5283..5487 of consensus"
repeat_region   111622..112876
                /note="L1MB8 repeat: matches 4877..6173 of consensus"
repeat_region   112873..114198
                /note="L1M4 repeat: matches 3073..4391 of consensus"
repeat_region   114206..115694
                /note="L1PA2 repeat: matches 4656..6144 of consensus"
repeat_region   115723..116219
                /note="MLT2CA repeat: matches 1..489 of consensus"
repeat_region   116220..116291
                /note="3 copies 24 mer 81% conserved"
repeat_region   116283..116348
                /note="MLT2CA repeat: matches 444..508 of consensus"
repeat_region   116377..118409
                /note="L1MEc repeat: matches 1212..2985 of consensus"
repeat_region   118410..118683
                /note="AluY repeat: matches 1..298 of consensus"
repeat_region   118684..118923
                /note="L1MEc repeat: matches 983..1212 of consensus"
repeat_region   118955..119117
                /note="MER20 repeat: matches 51..218 of consensus"
repeat_region   119118..119284
                /note="L1MEc repeat: matches 802..988 of consensus"
repeat_region   119285..119682
                /note="MLT1A1 repeat: matches 1..365 of consensus"
repeat_region   119683..119810
                /note="L1MEc repeat: matches 681..802 of consensus"
repeat_region   119830..120493
                /note="L2 repeat: matches 1734..2603 of consensus"
repeat_region   120522..120894
```

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                /note="MLT1B repeat: matches 1..426 of consensus"
repeat_region   120923..121042
                /note="5 copies 24 mer 68% conserved"
repeat_region   121180..121227
                /note="2 copies 24 mer 95% conserved"
repeat_region   121184..121227
                /note="22 copies 2 mer gt 100% conserved"
repeat_region   122617..122772
                /note="MER5A repeat: matches 4..188 of consensus"
repeat_region   122787..122900
                /note="MER5B repeat: matches 91..173 of consensus"
repeat_region   122901..123193
                /note="AluJo repeat: matches 4..298 of consensus"
repeat_region   123194..123275
                /note="MER5B repeat: matches 1..91 of consensus"
repeat_region   123437..124087
                /note="L2 repeat: matches 1555..2750 of consensus"
repeat_region   124164..124586
                /note="L2 repeat: matches 57..485 of consensus"
repeat_region   125405..125535
                /note="Charlie4a repeat: matches 369..495 of consensus"
repeat_region   125536..125695
                /note="FRAM repeat: matches 2..161 of consensus"
repeat_region   125696..126026
                /note="Charlie4a repeat: matches 19..369 of consensus"
repeat_region   126098..126459
                /note="MLT1A1 repeat: matches 1..365 of consensus"
repeat_region   126630..126693
                /note="L2 repeat: matches 2641..2704 of consensus"
repeat_region   126784..127362
                /note="L2 repeat: matches 2176..2750 of consensus"
repeat_region   127366..127489
                /note="MIR repeat: matches 46..185 of consensus"
repeat_region   127679..127826
                /note="L2 repeat: matches 2552..2691 of consensus"
repeat_region   127827..128126
                /note="AluJo repeat: matches 4..302 of consensus"
repeat_region   128127..128405
                /note="L2 repeat: matches 2241..2552 of consensus"
repeat_region   128518..128663
                /note="L2 repeat: matches 1873..2021 of consensus"
repeat_region   128674..129015
                /note="MLT1A1 repeat: matches 1..358 of consensus"
repeat_region   129016..129205
                /note="L2 repeat: matches 1672..1868 of consensus"
repeat_region   129216..129297
                /note="L2 repeat: matches 2639..2710 of consensus"
repeat_region   129340..129554
                /note="MIR repeat: matches 53..260 of consensus"
repeat_region   129661..129924
                /note="MIR repeat: matches 2..261 of consensus"
repeat_region   131041..131232
                /note="AluSg/x repeat: matches 135..292 of consensus"
repeat_region   131267..131548
                /note="AluY repeat: matches 18..311 of consensus"
repeat_region   131743..132226
                /note="MLT1G repeat: matches 31..496 of consensus"
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repeat_region   132996..133294
                /note="AluSx repeat: matches 1..298 of consensus"
repeat_region   133642..133701
                /note="MIR repeat: matches 69..128 of consensus"
repeat_region   134184..134313
                /note="L1P3 repeat: matches 5682..5809 of consensus"
repeat_region   134373..134437
                /note="L1MA7 repeat: matches 6224..6288 of consensus"
repeat_region   134438..134744
                /note="MER2 repeat: matches 34..345 of consensus"
repeat_region   134748..134835
                /note="L1MA6 repeat: matches 6154..6241 of consensus"
repeat_region   134878..135187
                /note="AluSx repeat: matches 1..310 of consensus"
repeat_region   135493..135866
                /note="L1MD2 repeat: matches 5962..6340 of consensus"
repeat_region   135888..136007
                /note="L1ME1 repeat: matches 6026..6135 of consensus"
repeat_region   136270..136561
                /note="AluSx repeat: matches 21..312 of consensus"
repeat_region   136598..136661
                /note="MIR repeat: matches 69..132 of consensus"
repeat_region   136902..137090
                /note="MIR repeat: matches 12..206 of consensus"
repeat_region   137099..137227
                /note="MLT1D repeat: matches 1..130 of consensus"
repeat_region   137228..137524
                /note="AluSx repeat: matches 1..296 of consensus"
repeat_region   137525..137870
                /note="MLT1D repeat: matches 130..471 of consensus"
repeat_region   137893..138056
                /note="AluJo repeat: matches 123..301 of consensus"
repeat_region   138057..138345
                /note="AluSx repeat: matches 5..292 of consensus"
repeat_region   138346..138472
                /note="AluJo repeat: matches 1..123 of consensus"
repeat_region   138474..138539
                /note="MLT1D repeat: matches 440..505 of consensus"
repeat_region   138554..138675
                /note="L2 repeat: matches 2066..2187 of consensus"
repeat_region   138694..139033
                /note="L2 repeat: matches 2362..2692 of consensus"
repeat_region   138993..139044
                /note="MIR repeat: matches 210..261 of consensus"
repeat_region   139737..139807
                /note="MLT1C repeat: matches 393..464 of consensus"
repeat_region   139808..139873
                /note="L1PA8 repeat: matches 6097..6162 of consensus"
repeat_region   139874..140272
                /note="MLT1C repeat: matches 1..393 of consensus"
repeat_region   140332..140461
                /note="MER5A repeat: matches 26..189 of consensus"
repeat_region   140611..140903
                /note="LTR16C repeat: matches 61..387 of consensus"
repeat_region   141410..141594
                /note="MIR repeat: matches 25..210 of consensus"
repeat_region   142664..142699
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                     /note="18 copies 2 mer tc 100% conserved"
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                     /note="AluSc repeat: matches 1..278 of consensus"
     repeat_region   143097..143180
                     /note="L2 repeat: matches 2643..2749 of consensus"
     repeat_region   143339..143662
                     /note="MLT1A1 repeat: matches 6..365 of consensus"
     repeat_region   143783..143885
                     /note="L2 repeat: matches 2593..2702 of consensus"
     repeat_region   145806..145889
                     /note="MIR repeat: matches 37..130 of consensus"
     repeat_region   145957..146261
                     /note="AluSq repeat: matches 1..308 of consensus"
     repeat_region   146264..146376
                     /note="MIR repeat: matches 117..235 of consensus"
     repeat_region   147583..147657
                     /note="L2 repeat: matches 2422..2502 of consensus"
     repeat_region   147859..147978
                     /note="L2 repeat: matches 2616..2750 of consensus"
     repeat_region   148013..148084
                     /note="L2 repeat: matches 2636..2707 of consensus"
     repeat_region   148687..149141
                     /note="LTR16B repeat: matches 1..461 of consensus"
     repeat_region   150442..151102
                     /note="L2 repeat: matches 1490..2109 of consensus"
BASE COUNT
ORIGIN

468 100   0.0
AF195953    Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene,
          complete cds. 206618 bp, DNA, linear, PRI 26-MAR-2002
ACCESSION   AF195953
VERSION     AF195953.2  GI:19718557
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 206618)
  AUTHORS   Ryan,J.W., Jin,L., Horvath,I. and Sprinkle,T.J.C.
  TITLE     Human membrane-bound aminopeptidase P genomic DNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 206618)
  AUTHORS   Ryan,J.W., Jin,L., Horvath,I. and Sprinkle,T.J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) Vascular Biology Center, Medical College of
          Georgia, 1120 15th Street, Augusta, GA 30912, USA
REFERENCE   3  (bases 1 to 206618)
  AUTHORS   Ryan,J.W., Jin,L., Horvath,I. and Sprinkle,T.J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Vascular Biology Center, Medical College of
          Georgia, 1120 15th Street, Augusta, GA 30912, USA
  REMARK    Sequence update by submitter
COMMENT     On Mar 26, 2002 this sequence version replaced gi:11066156.
FEATURES             Location/Qualifiers
     source          1..206618
                     /organism="Homo sapiens"
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene              144189..176791
                     /gene="XNPEP2"
     mRNA              join(144189..144502,147348..147421,149203..149313,
                     150445..150508,151478..151582,151837..151923,
                     152849..152995,155710..155811,156987..157068,
                     157392..157587,158401..158490,159714..159823,
                     160536..160613,161726..161797,164422..164482,
                     165754..165823,166414..166518,167248..167307,
                     167936..168012,172845..172934,173533..176791)
                     /gene="XNPEP2"
                     /product="membrane-bound aminopeptidase P"
     5'UTR             144189..144453
                     /gene="XNPEP2"
     CDS               join(144454..144502,147348..147421,149203..149313,
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                     157392..157587,158401..158490,159714..159823,
                     160536..160613,161726..161797,164422..164482,
                     165754..165823,166414..166518,167248..167307,
                     167936..168012,172845..172934,173533..173727)
                     /gene="XNPEP2"
                     /codon_start=1
                     /product="membrane-bound aminopeptidase P"
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                     /db_xref="GI:11066157"
     misc_feature      160606..160608
                     /gene="XNPEP2"
                     /note="putative proton shuttle; unclassified site"
     misc_feature      161778..161780
                     /gene="XNPEP2"
                     /note="divalent metal ligand; metal-binding site"
     misc_feature      164435..164437
                     /gene="XNPEP2"
                     /note="divalent metal ligand; metal-binding site"
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                     /gene="XNPEP2"
                     /note="divalent metal ligand; metal-binding site"
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                     /gene="XNPEP2"
                     /note="divalent metal ligand; metal-binding site"
     misc_feature      167977..167979
                     /gene="XNPEP2"
                     /note="divalent metal ligand; metal-binding site"
     3'UTR             175728..176791
                     /gene="XNPEP2"
BASE COUNT
ORIGIN

467  99   0.0
P_AAH14799  Human cDNA sequence SEQ ID NO:12589. 243 bp, cDNA, PAT 26-JUN-2001
ACCESSION   P_AAH14799
KEYWORDS    GENESEQ; Human; primer; detection; diagnosis; antisense therapy;
          gene therapy;  patent; patentdb (v200414, 01-JUL-2004).
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens.
```

REFERENCE 1 (bases 1 to 2243)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J. Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Otsuki,T.
TITLE Primer sets for synthesizing polynucleotides, particularly the 5602 full- length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
JOURNAL Patent: EP1074617-A2; Filing Date: 28-JUL-2000; 2000EP-00116126; Publication Date: 07-FEB-2001; Priority: 29-JUL-1999; 99JP-00248036. 27-AUG-1999; 99JP-00300253. 11-JAN-2000; 2000JP-00118776. 02-MAY-2000; 2000JP-00183767. 09-JUN-2000; 2000JP-00241899; Assignee: (HELI-) HELIX RES INST; Cross Reference: WPI; 2001-318749/34; Patent Format: Claim 8; SEQ ID NO 12589; 2537pp + Sequence Listing; English.
COMMENT The present invention describes primer sets for synthesising 5602 full- length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention
FEATURES Location/Qualifiers
BASE COUNT 467 a 630 c 637 g 509 t
ORIGIN

467 99 0.0
AK001855 Homo sapiens cDNA FLJ10993 fis, clone PLACE1002140. 2243 bp, mRNA, linear, PRI 30-JAN-2004
ACCESSION AK001855
VERSION AK001855.1 GI:7023382
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,

Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.

TITLE Complete sequencing and characterization of 21,243 full-length human cDNAs

JOURNAL Nat. Genet. 36 (1), 40-45 (2004)

PUBMED 14702039

REFERENCE 2

AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 2243)

AUTHORS Isogai,T. and Otsuki,T.

TITLE Direct Submission

JOURNAL Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES Location/Qualifiers

source 1..2243

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="PLACE1002140"

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                     /tissue_type="placenta"
                     /clone_lib="PLACE1"
                     /note="cloning vector: pME18SFL3"
     CDS             6..374
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="BAA91944.1"
                     /db_xref="GI:7023383"
BASE COUNT
ORIGIN

449  98   0.0
AX332625    Sequence 3134 from Patent WO0194629. 458 bp,
          DNA, linear, PAT 09-JAN-2002
ACCESSION   AX332625
VERSION     AX332625.1  GI:18123259
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
          Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
          gene sets
  JOURNAL   Patent: WO 0194629-A 3134 13-DEC-2001;
          Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1..458
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
BASE COUNT
ORIGIN

449  98   0.0
AX332852    Sequence 3361 from Patent WO0194629. 458 bp,
          DNA, linear, PAT 09-JAN-2002
ACCESSION   AX332852
VERSION     AX332852.1  GI:18123486
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
          Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
          gene sets
  JOURNAL   Patent: WO 0194629-A 3361 13-DEC-2001;
          Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1..458
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                     /mol_type="unassigned DNA"
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/db_xref="taxon:9606"

BASE COUNT
ORIGIN

Dayhoff Protein Database (Rel 78, Mar 2004)

P_AAB87540 Human PRO831 - Homo sapiens.
Length: 73 aa
Accession: P_AAB87540;
Species: Homo sapiens.
Keywords: Human; PRO protein; mapping; patent; GENESEQ patentdb.
Patent number: WO200116318-A2.
Publication date: 08-MAR-2001.
Filing date: 24-AUG-2000; 2000WO-US023328.
Priority: 01-SEP-1999; 99WO-US020111. 15-SEP-1999; 99WO-US021090.
07-DEC-1999; 99US-0169495P. 09-DEC-1999; 99US-0170262P.
11-JAN-2000; 2000US-0175481P. 18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342. 22-FEB-2000; 2000WO-US004414.
01-MAR-2000; 2000WO-US005601. 03-MAR-2000; 2000US-0187202P.
21-MAR-2000; 2000US-0191007P. 30-MAR-2000; 2000WO-US008439.
25-APR-2000; 2000US-0199397P. 22-MAY-2000; 2000WO-US014042.
05-JUN-2000; 2000US-0209832P.
Assignee: (GETH) GENENTECH INC.
Inventors: Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
Cross reference: WPI; 2001-183260/18. N-PSDB; AAF92072.
Title: Eighty four nucleic acids encoding PRO polypeptides, useful in
molecular biology, including use as hybridization probes, and in
chromosome and gene mapping.
Patent format: Claim 12; Fig 30; 278pp; English.
Comment: The present sequence is a human PRO polypeptide (secreted and
transmembrane). The PRO protein, and PRO agonists, PRO antagonists
or anti-PRO antibodies are useful for preparation of a medicament
useful in the treatment of a condition which is responsive to the
PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
protein may also be employed as molecular weight markers for
protein electrophoresis. The PRO coding sequence has applications
in molecular biology, including use as hybridisation probes, and in
chromosome and gene mapping
Database: GENESEQ patent database (v200414, 01-JUL-2004).

P_AAY99346 Human PRO831 (UNQ471) amino acid sequence SEQ ID NO:22 - Homo
sapiens.
Length: 73 aa
Accession: P_AAY99346;
Species: Homo sapiens.
Keywords: Human; PRO polypeptide; membrane bound protein; receptor;
diagnosis; transmembrane; secretion; immunoadhesion;
pharmaceutical; screening; patent; GENESEQ patentdb.
Patent number: WO200012708-A2.
Publication date: 09-MAR-2000.
Filing date: 01-SEP-1999; 99WO-US020111.
Priority: 01-SEP-1998; 98US-0098716P. 01-SEP-1998; 98US-0098749P.
01-SEP-1998; 98US-0098750P.18-NOV-1998; 98US-0108858P. 18-NOV-1998;
98US-0108904P. plus 119 more dates.
Assignee: (GETH) GENENTECH INC.
Inventors: Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
Cross reference: WPI; 2000-237871/20. N-PSDB; AAA37028.
Title: New mammalian DNA sequences encoding transmembrane, receptor or
secreted PRO polypeptides, useful for screening of potential
peptide or small molecule inhibitors of the relevant

receptor/ligand interactions.
Patent format: Claim 12; Fig 14; 773pp; English.
Comment: AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention
Database: GENESEQ patent database (v200414, 01-JUL-2004).